

Db	11 MEFPKQOKVEDFYDIEGLSGQFATVKCREEKSGLEYAKFIKKRQSRASRGVSR 70	Qy	121 KOILDGVNLYHTKKTAHFDPENIMLLDKNIPIPHKLIDFGLAHEIDGVEFKNIFGT 180
Qy	61 IEREVSILROVLHNVITLHDYENRDTWHLILEVSGGELFLQKESEERATSFI 120	Db	131 KOILDGVNLYHTKKTAHFDPENIMLLDKNIPIPHKLIDFGLAHEIDGVEFKNIFGT 190
Db	71 IEREVSILROVLHNVITLHDYENRDTWHLILEVSGGELFLQKESEERATSFI 130	Qy	181 PEVVAPEIVNVEPLGLEADMSIGVITYILISGASPLGDTKQETLANITSVSYDEEF 240
Qy	121 KOILDGVNLYHTKKTAHFDPENIMLLDKNIPIPHKLIDFGLAHEIDGVEFKNIFGT 180	Db	191 PEVVAPEIVNVEPLGLEADMSIGVITYILISGASPLGDTKQETLANITSVSYDEEF 250
Db	131 KOILDGVNLYHTKKTAHFDPENIMLLDKNIPIPHKLIDFGLAHEIDGVEFKNIFGT 190	Qy	241 FSHTSPLAKDTIRKLKVKEKRKLTOEALRHWPITPVQDQAMTRRESVNLERFKQY 300
Qy	181 PEVVAPEIVNVEPLGLEADMSIGVITYILISGASPLGDTKQETLANITSVSYDEEF 240	Db	251 FSOTSPPLAKDTIRKLKVKEKRKLTOEALRHWPITPVQDQAMTRRESVNLERFKQY 310
Db	191 PEVVAPEIVNVEPLGLEADMSIGVITYILISGASPLGDTKQETLANITSVSYDEEF 250	Qy	301 VRRWKLSFSIVSLCNHLTSLMKVHLRDPEDLRNCESDEEDIARRKALHPRRSSTS 360
Qy	241 FSHTSPLAKDTIRKLKVKEKRKLTOEALRHWPITPVQDQAMTRRESVNLERFKQY 300	Db	311 VRRWKLSFSIVSLCNHLTSLMKVHLRDPEDLRNCESDEEDIARRKALHPRRSSTS 370
Db	251 FSOTSPPLAKDTIRKLKVKEKRKLTOEALRHWPITPVQDQAMTRRESVNLERFKQY 310	RESULT 2	36<
OQUIK4	PRELIMINARY; PRT; 370 AA.	OQOYM4	J2;
ID	OQUIK4	ID	OQOYM4
AC	OQUIK4	AC	OQOYM4
DT	01-MAY-2000 (TREMBLrel: 13, Created)	DT	01-MAY-2000 (TREMBLrel: 13, Last sequence update)
DT	01-MAY-2000 (TREMBLrel: 13, Last sequence update)	DT	01-DEC-2001 (TREMBLrel: 19, Last annotation update)
DE	DEATH-ASSOCIATED PROTEIN KINASE 2.	DE	DEATH ASSOCIATED PROTEIN KINASE 2.
GN	DAPK2.	GN	DAPK2 OR DAPK2.
OS	Homo sapiens (Human).	OS	Mus musculus (Mouse).
OC	Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominoide; Homo; NCBI_TaxID=9606;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathii; Murinae; Mus; NCBI_TaxID=1090;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N_A.	RP	SEQUENCE FROM N_A.
RX	MEDLINE=9903018; PubMed=10376525;	RX	MEDLINE=9903018; PubMed=10376525;
RX	Kawai T., Nomura F., Hoshino K., Copeland N.G., Gilbert D.J., Jenkins N.A., Akira S.;	RX	Kawai T., Nomura F., Hoshino K., Copeland N.G., Gilbert D.J., Jenkins N.A., Akira S.;
RA	"Death-associated protein kinase 2 is a new calcium/calmodulin-dependent protein kinase that signals apoptosis through its catalytic activity".	RA	"Death-associated protein kinase 2 is a new calcium/calmodulin-dependent protein kinase that signals apoptosis through its catalytic activity".
RT	Oncogene 18:3471-3480(1999).	RT	Oncogene 18:3471-3480(1999).
RL	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.	RL	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC	-	CC	-
DR	EMBL: AB018001; BAA88063.1; -	DR	EMBL: AB018002; BAA88064.1; -
DR	HSSP: Q63450; IA06.	DR	HSSP: Q63450; IA06.
DR	MGI:1341297; Dapk2.	DR	MGI:1341297; Dapk2.
DR	Interpro; IPR000719; Euk_pk kinase.	DR	Interpro; IPR000719; Ser_thr_pk kinase.
DR	Interpro; IPR002290; Ser_thr_pk kinase.	DR	Interpro; IPR002290; Ser_thr_pk kinase.
DR	Interpro; IPR001245; Tyr_pk kinase.	DR	Interpro; IPR001245; Tyr_pk kinase.
DR	PFam: PF00069; pk kinase; 1.	DR	PFam: PF00069; pk kinase; 1.
DR	PRINTS; PRO0109; TYRKINASE.	DR	PRINTS; PRO0109; TYRKINASE.
DR	SMART; SM00220; S_TKC; 1.	DR	SMART; SM00220; S_TKC; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS500108; PROTEIN_KINASE_SP; 1.	DR	PROSITE; PS500108; PROTEIN_KINASE_SP; 1.
DR	ATP-binding; Kinase; Serine/threonine-protein kinase; transferase.	DR	ATP-binding; Kinase; Serine/threonine-protein kinase; transferase.
KW	SEQUENCE 370 AA; 42898 MW; 0358914BBCD881A2 CRC64;	KW	SEQUENCE 370 AA; 42769 MW; 7DAE29C4E661B3 CRC64;
Query Match 98.8%; Score 1824; DB 4; Length 370; Best Local Similarity 99.2%; Pred. No. 26-124; Mismatches 357; Conservative 1; Indels 0; Gaps 0;	Query Match 95.6%; Score 1764; DB 11; Length 370; Best Local Similarity 96.4%; Pred. No. 4-4e-120; Mismatches 347; Conservative 4; Indels 9; Gaps 0;	Qy	1 MEFPKQOKVEDFYDIEGLSGQFATVKCREEKSGLEYAKFIKKRQSRASRGVSR 60
Qy	1 MEFPKQOKVEDFYDIEGLSGQFATVKCREEKSGLEYAKFIKKRQSRASRGVSR 60	Db	11 METPKQOKVEDFYDIEGLSGQFATVKCREEKSGLEYAKFIKKRQSRASRGVSR 70
Db	11 METPKQOKVEDFYDIEGLSGQFATVKCREEKSGLEYAKFIKKRQSRASRGVSR 70	Qy	61 IEREVSILROVLHNVITLHDYENRDTWHLILEVSGGELFLQKESEERATSFI 120
Qy	61 IEREVSILROVLHNVITLHDYENRDTWHLILEVSGGELFLQKESEERATSFI 120	Db	71 IEREVSILROVLHNVITLHDYENRDTWHLILEVSGGELFLQKESEERATSFI 130
Db	71 IEREVSILROVLHNVITLHDYENRDTWHLILEVSGGELFLQKESEERATSFI 130	Qy	121 KOILDGVNLYHTKKTAHFDPENIMLLDKNIPIPHKLIDFGLAHEIDGVEFKNIFGT 180
Db	131 KOILDGVNLYHTKKTAHFDPENIMLLDKNIPIPHKLIDFGLAHEIDGVEFKNIFGT 190	Db	131 KOILDGVNLYHTKKTAHFDPENIMLLDKNIPIPHKLIDFGLAHEIDGVEFKNIFGT 190